

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.**

Application Serial Number: 09/689,992C  
Source: 1FW16  
Date Processed by STIC: 11/10/04

# ***ENTERED***



IFW16

## RAW SEQUENCE LISTING

DATE: 11/10/2004

PATENT APPLICATION: US/09/689,992C

TIME: 15:41:19

Input Set : A:\seqlist corr.txt

Output Set : N:\CRF4\11102004\I689992C.raw

3 <110> APPLICANT: Mello, Craig C.  
 4 Tabara, Hiroaki  
 5 Grishok, Alla  
 6 Fire, Andrew  
 8 <120> TITLE OF INVENTION: RNA INTERFERENCE PATHWAY GENES AS TOOLS FOR TARGETED GENETIC  
 9 INTERFERENCE  
 11 <130> FILE REFERENCE: UMG-052  
 13 <140> CURRENT APPLICATION NUMBER: US 09/689,992C  
 14 <141> CURRENT FILING DATE: 2000-10-13  
 16 <150> PRIOR APPLICATION NUMBER: US 60/193,218  
 17 <151> PRIOR FILING DATE: 2000-03-30  
 19 <150> PRIOR APPLICATION NUMBER: US 60/159,776  
 20 <151> PRIOR FILING DATE: 1999-10-15  
 22 <160> NUMBER OF SEQ ID NOS: 14  
 24 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
 26 <210> SEQ ID NO: 1  
 27 <211> LENGTH: 3719  
 28 <212> TYPE: DNA  
 29 <213> ORGANISM: Caenorhabditis elegans  
 31 <400> SEQUENCE: 1  
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 33 gtcattctct cgatccggtg tgatcaatta ttagcagcta taagatatat aagtttgata 120  
 34 ttaatattat aggagatgaa atggcttgcg aggccactg gtaaagcgaa cggcaaattc 180  
 35 tatgagaaga aagtacttct tttggtaaat tggttcaagt tctccagcaa aattttacgat 240  
 36 cggaataact acgagtatga agtgaaaatg acaaaggaag tattgaatag aaaaccagga 300  
 37 aaacctttcc caaaaaagac agaaattcca atgtaagtgc ttgtaaatta gtcaaaaacta 360  
 38 atttttatctt tcagtcccga tcgtgcaaaa ctcttctggc aacatcttcg gcatgagaag 420  
 39 aagcagacag atttttattct cgaagactat gtttttgatg aaaaggacac tgtttatagt 480  
 40 gtttgcgcac tgaacactgt cacatcaaaa atgctggttt cggagaaaag agtaaaaaag 540  
 41 gattcggaga aaaaagatga aaaggatttg gagaaaaaaa tcttatacac aatgatactt 600  
 42 acctatcgta aaaaatttca cctgaacttt agtcgagaaa atccggaaaa agacgaagaa 660  
 43 gcgaatcgga gttacaaatt cctgaagggt tatgaaaaac acgcattata acaaacaaaa 720  
 44 ttagctttca gaatgttatg acccagaaag ttcgctacgc gccttttggtg aacgaggaga 780  
 45 ttaaagtgtg agttgcaata ataataataa taatcacctc aactcattta tatattttta 840  
 46 gacaattcgc gaaaaatttt gtgtacgata ataattcaat tctgcgagtt cctgaatcgt 900  
 47 ttcacgatcc aaacagattc gaacaatcat tagaagtagc accaagaatc gaagcatggt 960  
 48 ttggaattta cattggaatc aaagaattgt tcgatgggtg acctgtgctc aattttgcaa 1020  
 49 gtaagtttga gaaactgcga taaaaaatca tgtgattttt gttgaagttg tcgataaaact 1080  
 50 attctacaat gcaccgaaaa tgtctcttct ggattatctt ctcttaattg tcgaccccca 1140  
 51 gtcgtgtaac gatgatgtac gaaaagatct taaaacaaaa ctgatggcgg gaaaaatgac 1200  
 52 aatcagacaa gccgcgcggc caagaattcg acaattattg gaaaatttga agctgaaatg 1260  
 53 cgcagaagtt tgggataacg aaatgttagt tttaaattatt caaacaatta atatacaaat 1320  
 54 tgattttcag gtcgagattg acagaacgac atctgacatt tctagatttg tgcgaggaaa 1380

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55 actctcttgt ttataaagtc actggtaaat cggacagagg aagaaatgca aaaaagtacg 1440
56 atactacatt gttcaaaatc tatgaggaaa acaaaaagtt cattgagttt cccacctac 1500
57 cactagtcaa agttaaaggt ggagcaaaag aatacgctgt accaatggaa catcttgaag 1560
58 ttcatgagaa gccacaaaga tacaagaatc gaattgatct ggtgatgcaa gacaagtttc 1620
59 taaagcgagc tacacgaaaa cctcacgact acaaagaaaa taccctaaaa atgctgaaa 1680
60 aattggattt ctcttctgaa gagctaaatt ttggtgaaag atttggatta tgctccaaac 1740
61 ttcagatgat cgaatgtcca ggaaagggtt tgaaagagcc aatgcttgtg aatagtgtaa 1800
62 atgaacaaat taaaatgaca ccagtgtatt gtggatttca agaaaaacaa ttgaatgtgg 1860
63 ttcccgaaaa agaactttgc tgtgctgttt ttgtagtcaa cgaaacagcg ggaaatccat 1920
64 gcttagaaga gaacgacgtt gtgtaagtgt ttctacgta gattattccg aaatattttc 1980
65 agtaagttct acaccgaact aattggtggt tgcaagttcc gtggaatacg aattggtgcc 2040
66 aatgaaaaca gaggacgca atctattatg tacgacgca cgaaaaatga atatgccgta 2100
67 agtttcagaa aattgaaagt ttttaaatat catatttaca gttctacaaa aattgtacac 2160
68 taaataccgg aatcggtaga tttgaaatag ccgcaacaga agcgaagaat atgtttgaac 2220
69 gtcttcccga taaagaacaa aaagtcttaa tgttcattat catttccaaa cgacaactga 2280
70 atgcttacgg ttttgtgaaa cattattgag atcacaccat cgggtgtagt aatcagcata 2340
71 ttacttctga aacagtcaca aaagctttgg catcactaag gcacgagaaa ggatcaaaac 2400
72 gaattttcta tcaaattgca ttgaaaatca acgcgaaatt aggaggtatt aaccaggagc 2460
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75 attctatagc ggctgtagta gcgagtatca atccagggtg aactatctat cgaaatatga 2640
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78 ttgagtattt aaaagatctc tgggattttt aatttttttg taaactttca gaacaacgac 2820
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81 cgggatggag aagatccaga gccgaagtac acgttcattg tgattcagaa aagacacaat 3000
82 acacgattgc ttcgaagaat ggaaaaagat aagccagtgg tcaataaaga tcttactcct 3060
83 gctgaaacag atgtcgctgt tgctgctgtt aaacaatggg aggaggatat gaaagaaagc 3120
84 aaagaaactg gaattgtgaa cccatcatcc ggaacaactg tggataaact tatcgtttcg 3180
85 aaatacaaat tcgatttttt cttggcatct catcatggtg tccttggtac atctcgtcca 3240
86 ggacattaca ctgttatgta tgacgataaa ggaatgagcc aagatgaagt ctatgtaagc 3300
87 gttttgaata gcagttagcg atttttaggat tttgtaatcc gcatatagtt attataaaaa 3360
88 aatgtttcag aaaatgacct acggacttgc ttttctctct gctagatgtc gaaaaccct 3420
89 ctcgttgcct gttccggttc attatgctca tttatcatgt gaaaaagcga aagagcttta 3480
90 tcgaacttac aaggaacatt acatcggtga ctatgcacag ccacggactc gacacgaaat 3540
91 ggaacatttt ctccaaacta acgtgaagta ccttgaatg tcgttcgcat aacattttgc 3600
92 aaaagtgtcg ccggtttcaa tcaaattttt caattgtaga tattgtactt actttttttt 3660
93 aaagcccggt ttcaaaaatt cattccatga ctaacgtttt cataaattac ttgaaattt 3719
95 <210> SEQ ID NO: 2
96 <211> LENGTH: 3227
97 <212> TYPE: DNA
98 <213> ORGANISM: Caenorhabditis elegans
100 <220> FEATURE:
101 <221> NAME/KEY: CDS
102 <222> LOCATION: (21)...(3080)
104 <400> SEQUENCE: 2
105 cagccacaaa gtgatgaaac atg tcc tcg aat ttt ccc gaa ttg gaa aaa gga 53
106 Met Ser Ser Asn Phe Pro Glu Leu Glu Lys Gly

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107						1				5				10			
109	ttt	tat	cgt	cat	tct	ctc	gat	ccg	gag	atg	aaa	tgg	ctt	gcg	agg	ccc	101
110	Phe	Tyr	Arg	His	Ser	Leu	Asp	Pro	Glu	Met	Lys	Trp	Leu	Ala	Arg	Pro	
111				15					20				25				
113	act	ggt	aaa	tgc	gac	ggc	aaa	ttc	tat	gag	aag	aaa	gta	ctt	ctt	ttg	149
114	Thr	Gly	Lys	Cys	Asp	Gly	Lys	Phe	Tyr	Glu	Lys	Lys	Val	Leu	Leu	Leu	
115			30					35					40				
117	gta	aat	tgg	ttc	aag	ttc	tcc	agc	aaa	att	tac	gat	cgg	gaa	tac	tac	197
118	Val	Asn	Trp	Phe	Lys	Phe	Ser	Lys	Ile	Tyr	Asp	Arg	Glu	Tyr	Tyr		
119		45					50				55						
121	gag	tat	gaa	gtg	aaa	atg	aca	aag	gaa	gta	ttg	aat	aga	aaa	cca	gga	245
122	Glu	Tyr	Glu	Val	Lys	Met	Thr	Lys	Glu	Val	Leu	Asn	Arg	Lys	Pro	Gly	
123	60				65				70				75				
125	aaa	cct	ttc	cca	aaa	aag	aca	gaa	att	cca	att	ccc	gat	cgt	gca	aaa	293
126	Lys	Pro	Phe	Pro	Lys	Lys	Thr	Glu	Ile	Pro	Ile	Pro	Asp	Arg	Ala	Lys	
127				80				85				90					
129	ctc	ttc	tgg	caa	cat	ctt	cgg	cat	gag	aag	aag	cag	aca	gat	ttt	att	341
130	Leu	Phe	Trp	Gln	His	Leu	Arg	His	Glu	Lys	Lys	Gln	Thr	Asp	Phe	Ile	
131			95				100				105						
133	ctc	gaa	gac	tat	gtt	ttt	gat	gaa	aag	gac	act	gtt	tat	agt	gtt	tgt	389
134	Leu	Glu	Asp	Tyr	Val	Phe	Asp	Glu	Lys	Asp	Thr	Val	Tyr	Ser	Val	Cys	
135		110				115					120						
137	cga	ctg	aac	act	gtc	aca	tca	aaa	atg	ctg	gtt	tcg	gag	aaa	gta	gta	437
138	Arg	Leu	Asn	Thr	Val	Thr	Ser	Lys	Met	Leu	Val	Ser	Glu	Lys	Val	Val	
139		125				130					135						
141	aaa	aag	gat	tcg	gag	aaa	aaa	gat	gaa	aag	gat	ttg	gag	aaa	aaa	atc	485
142	Lys	Lys	Asp	Ser	Glu	Lys	Lys	Asp	Glu	Lys	Asp	Leu	Glu	Lys	Lys	Ile	
143	140				145				150				155				
145	tta	tac	aca	atg	ata	ctt	acc	tat	cgt	aaa	aaa	ttt	cac	ctg	aac	ttt	533
146	Leu	Tyr	Thr	Met	Ile	Leu	Thr	Tyr	Arg	Lys	Lys	Phe	His	Leu	Asn	Phe	
147			160				165				170						
149	agt	cga	gaa	aat	ccg	gaa	aaa	gac	gaa	gaa	gcg	aat	cgg	agt	tac	aaa	581
150	Ser	Arg	Glu	Asn	Pro	Glu	Lys	Asp	Glu	Glu	Ala	Asn	Arg	Ser	Tyr	Lys	
151			175				180				185						
153	ttc	ctg	aag	aat	gtt	atg	acc	cag	aaa	gtt	cgc	tac	gcg	cct	ttt	gtg	629
154	Phe	Leu	Lys	Asn	Val	Met	Thr	Gln	Lys	Val	Arg	Tyr	Ala	Pro	Phe	Val	
155		190				195					200						
157	aac	gag	gag	att	aaa	gta	caa	ttc	gcg	aaa	aat	ttt	gtg	tac	gat	aat	677
158	Asn	Glu	Glu	Ile	Lys	Val	Gln	Phe	Ala	Lys	Asn	Phe	Val	Tyr	Asp	Asn	
159		205			210				215								
161	aat	tca	att	ctg	cga	gtt	cct	gaa	tcg	ttt	cac	gat	cca	aac	aga	ttc	725
162	Asn	Ser	Ile	Leu	Arg	Val	Pro	Glu	Ser	Phe	His	Asp	Pro	Asn	Arg	Phe	
163	220				225				230				235				
165	gaa	caa	tca	tta	gaa	gta	gca	cca	aga	atc	gaa	gca	tgg	ttt	gga	att	773
166	Glu	Gln	Ser	Leu	Glu	Val	Ala	Pro	Arg	Ile	Glu	Ala	Trp	Phe	Gly	Ile	
167			240				245				250						
169	tac	att	gga	atc	aaa	gaa	ttg	ttc	gat	ggg	gaa	cct	gtg	ctc	aat	ttt	821
170	Tyr	Ile	Gly	Ile	Lys	Glu	Leu	Phe	Asp	Gly	Glu	Pro	Val	Leu	Asn	Phe	
171			255				260				265						

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173	gca att gtc gat aaa cta ttc tac aat gca ccg aaa atg tct ctt ctg	869
174	Ala Ile Val Asp Lys Leu Phe Tyr Asn Ala Pro Lys Met Ser Leu Leu	
175	270 275 280	
177	gat tat ctt ctc cta att gtc gac ccc cag tcg tgt aac gat gat gta	917
178	Asp Tyr Leu Leu Leu Ile Val Asp Pro Gln Ser Cys Asn Asp Asp Val	
179	285 290 295	
181	cga aaa gat ctt aaa aca aaa ctg atg gcg gga aaa atg aca atc aga	965
182	Arg Lys Asp Leu Lys Thr Lys Leu Met Ala Gly Lys Met Thr Ile Arg	
183	300 305 310 315	
185	caa gcc gcg cgg cca aga att cga caa tta ttg gaa aat ttg aag ctg	1013
186	Gln Ala Ala Arg Pro Arg Ile Arg Gln Leu Leu Glu Asn Leu Lys Leu	
187	320 325 330	
189	aaa tgc gca gaa gtt tgg gat aac gaa atg tcg aga ttg aca gaa cga	1061
190	Lys Cys Ala Glu Val Trp Asp Asn Glu Met Ser Arg Leu Thr Glu Arg	
191	335 340 345	
193	cat ctg aca ttt cta gat ttg tgc gag gaa aac tct ctt gtt tat aaa	1109
194	His Leu Thr Phe Leu Asp Leu Cys Glu Glu Asn Ser Leu Val Tyr Lys	
195	350 355 360	
197	gtc act ggt aaa tcg gac aga gga aga aat gca aaa aag tac gat act	1157
198	Val Thr Gly Lys Ser Asp Arg Gly Arg Asn Ala Lys Lys Tyr Asp Thr	
199	365 370 375	
201	aca ttg ttc aaa atc tat gag gaa aac aaa aag ttc att gag ttt ccc	1205
202	Thr Leu Phe Lys Ile Tyr Glu Glu Asn Lys Lys Phe Ile Glu Phe Pro	
203	380 385 390 395	
205	cac cta cca cta gtc aaa gtt aaa agt gga gca aaa gaa tac gct gta	1253
206	His Leu Pro Leu Val Lys Val Lys Ser Gly Ala Lys Glu Tyr Ala Val	
207	400 405 410	
209	cca atg gaa cat ctt gaa gtt cat gag aag cca caa aga tac aag aat	1301
210	Pro Met Glu His Leu Glu Val His Glu Lys Pro Gln Arg Tyr Lys Asn	
211	415 420 425	
213	cga att gat ctg gtg atg caa gac aag ttt cta aag cga gct aca cga	1349
214	Arg Ile Asp Leu Val Met Gln Asp Lys Phe Leu Lys Arg Ala Thr Arg	
215	430 435 440	
217	aaa cct cac gac tac aaa gaa aat acc cta aaa atg ctg aaa gaa ttg	1397
218	Lys Pro His Asp Tyr Lys Glu Asn Thr Leu Lys Met Leu Lys Glu Leu	
219	445 450 455	
221	gat ttc tct tct gaa gag cta aat ttt gtt gaa aga ttt gga tta tgc	1445
222	Asp Phe Ser Ser Glu Glu Leu Asn Phe Val Glu Arg Phe Gly Leu Cys	
223	460 465 470 475	
225	tcc aaa ctt cag atg atc gaa tgt cca gga aag gtt ttg aaa gag cca	1493
226	Ser Lys Leu Gln Met Ile Glu Cys Pro Gly Lys Val Leu Lys Glu Pro	
227	480 485 490	
229	atg ctt gtg aat agt gta aat gaa caa att aaa atg aca cca gtg att	1541
230	Met Leu Val Asn Ser Val Asn Glu Gln Ile Lys Met Thr Pro Val Ile	
231	495 500 505	
233	cgt gga ttt caa gaa aaa caa ttg aat gtg gtt ccc gaa aaa gaa ctt	1589
234	Arg Gly Phe Gln Glu Lys Gln Leu Asn Val Val Pro Glu Lys Glu Leu	
235	510 515 520	
237	tgc tgt gct gtt ttt gta gtc aac gaa aca gcg gga aat cca tgc tta	1637

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238	Cys	Cys	Ala	Val	Phe	Val	Val	Asn	Glu	Thr	Ala	Gly	Asn	Pro	Cys	Leu	
239		525					530					535					
241	gaa	gag	aac	gac	gtt	gtt	aag	ttc	tac	acc	gaa	cta	att	ggt	ggt	tgc	1685
242	Glu	Glu	Asn	Asp	Val	Val	Lys	Phe	Tyr	Thr	Glu	Leu	Ile	Gly	Gly	Cys	
243	540					545					550					555	
245	aag	ttc	cgt	gga	ata	cga	att	ggt	gcc	aat	gaa	aac	aga	gga	gcg	caa	1733
246	Lys	Phe	Arg	Gly	Ile	Arg	Ile	Gly	Ala	Asn	Glu	Asn	Arg	Gly	Ala	Gln	
247					560					565					570		
249	tct	att	atg	tac	gac	gcg	acg	aaa	aat	gaa	tat	gcc	ttc	tac	aaa	aat	1781
250	Ser	Ile	Met	Tyr	Asp	Ala	Thr	Lys	Asn	Glu	Tyr	Ala	Phe	Tyr	Lys	Asn	
251				575					580					585			
253	tgt	aca	cta	aat	acc	gga	atc	ggt	aga	ttt	gaa	ata	gcc	gca	aca	gaa	1829
254	Cys	Thr	Leu	Asn	Thr	Gly	Ile	Gly	Arg	Phe	Glu	Ile	Ala	Ala	Thr	Glu	
255			590					595					600				
257	gcg	aag	aat	atg	ttt	gaa	cgt	ctt	ccc	gat	aaa	gaa	caa	aaa	gtc	tta	1877
258	Ala	Lys	Asn	Met	Phe	Glu	Arg	Leu	Pro	Asp	Lys	Glu	Gln	Lys	Val	Leu	
259		605				610					615						
261	atg	ttc	att	atc	att	tcc	aaa	cga	caa	ctg	aat	gct	tac	ggt	ttt	gtg	1925
262	Met	Phe	Ile	Ile	Ile	Ser	Lys	Arg	Gln	Leu	Asn	Ala	Tyr	Gly	Phe	Val	
263	620					625				630						635	
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266	Lys	His	Tyr	Cys	Asp	His	Thr	Ile	Gly	Val	Ala	Asn	Gln	His	Ile	Thr	
267				640						645				650			
269	tct	gaa	aca	gtc	aca	aaa	gct	ttg	gca	tca	cta	agg	cac	gag	aaa	gga	2021
270	Ser	Glu	Thr	Val	Thr	Lys	Ala	Leu	Ala	Ser	Leu	Arg	His	Glu	Lys	Gly	
271			655						660					665			
273	tca	aaa	cga	att	ttc	tat	caa	att	gca	ttg	aaa	atc	aac	gcg	aaa	tta	2069
274	Ser	Lys	Arg	Ile	Phe	Tyr	Gln	Ile	Ala	Leu	Lys	Ile	Asn	Ala	Lys	Leu	
275			670						675				680				
277	gga	ggt	att	aac	cag	gag	ctt	gac	tgg	tca	gaa	att	gca	gaa	ata	tca	2117
278	Gly	Gly	Ile	Asn	Gln	Glu	Leu	Asp	Trp	Ser	Glu	Ile	Ala	Glu	Ile	Ser	
279		685				690					695						
281	cca	gaa	gaa	aaa	gaa	aga	cgg	aaa	aca	atg	cca	tta	act	atg	tat	gtt	2165
282	Pro	Glu	Glu	Lys	Glu	Arg	Arg	Lys	Thr	Met	Pro	Leu	Thr	Met	Tyr	Val	
283	700					705					710					715	
285	gga	att	gat	gta	act	cat	cca	acc	tcc	tac	agt	gga	att	gat	tat	tct	2213
286	Gly	Ile	Asp	Val	Thr	His	Pro	Thr	Ser	Tyr	Ser	Gly	Ile	Asp	Tyr	Ser	
287				720						725				730			
289	ata	gcg	gct	gta	gta	gcg	agt	atc	aat	cca	ggt	gga	act	atc	tat	cga	2261
290	Ile	Ala	Ala	Val	Val	Ala	Ser	Ile	Asn	Pro	Gly	Gly	Thr	Ile	Tyr	Arg	
291			735						740				745				
293	aat	atg	att	gtg	act	caa	gaa	gaa	tgt	cgt	ccc	ggt	gag	cgt	gca	gtg	2309
294	Asn	Met	Ile	Val	Thr	Gln	Glu	Glu	Cys	Arg	Pro	Gly	Glu	Arg	Ala	Val	
295			750						755				760				
297	gct	cat	gga	cgg	gaa	aga	aca	gat	att	ttg	gaa	gca	aag	ttc	gtg	aaa	2357
298	Ala	His	Gly	Arg	Glu	Arg	Thr	Asp	Ile	Leu	Glu	Ala	Lys	Phe	Val	Lys	
299		765					770					775					
301	ttg	ctc	aga	gaa	ttc	gca	gaa	aac	aac	gac	aat	cga	gca	cca	gcg	cat	2405
302	Leu	Leu	Arg	Glu	Phe	Ala	Glu	Asn	Asn	Asp	Asn	Arg	Ala	Pro	Ala	His	

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:8; Xaa Pos. 2,3,4,6,8,9,10,12,13,14,15,16,17,18,19,21,22,23,24,25,26

Seq#:8; Xaa Pos. 29,31,32,33,35,36,37,39,40,41,43,44,45,46,47,49,51,55,56

Seq#:8; Xaa Pos. 59,60,63,64,67,68

VERIFICATION SUMMARY

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TIME: 15:41:20

Input Set : A:\seqlist corr.txt

Output Set: N:\CRF4\11102004\I689992C.raw

L:794 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!  
L:798 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:8  
L:799 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:0  
M:341 Repeated in SeqNo=8